The embodiments of the invention in which an exclusive property or privilege is claimed are defined as follows:

1. A method of identifying genetic mutations that are associated with ataxic neurological disease in a mammalian subject, said method comprising identifying a difference between a nucleic acid sequence of a protein kinase C gamma gene from a first mammalian subject exhibiting ataxia and a nucleic acid sequence of a protein kinase C gamma gene from a second mammalian subject which is not exhibiting ataxia, wherein the first and second mammalian subjects are members of the same species, and wherein the difference between the nucleic acid sequences is a genetic mutation that is associated with ataxic neurological disease.

2. The method of Claim 1 wherein the nucleic acid sequence of said first subject and said second subject is determined by amplification of portions of protein kinase C gamma genes from genomic DNA isolated from said subjects to produce an amplified DNA and sequencing said amplified DNA.

3. The method of Claim 1 further comprising determining whether the identified genetic mutations cosegregate with ataxia observed in the subjects suffering from ataxia.

4. The method of Claim 3 wherein said cosegregation is detected by a method selected from the group consisting of direct sequencing, sequencing PCR-amplified DNA, single stranded conformation analysis, allele-specific PCR and restriction fragment length polymorphism.

5. The method of Claim 4 wherein said cosegregation is detected by sequencing PCR-amplified DNA.

6. The method of Claim 4 wherein said cosegregation is detected by restriction fragment length polymorphism wherein the presence of an aberrant restriction enzyme site is indicative of the presence of said genetic mutation and cosegregation is determined by the presence of said genetic mutation in a first population of mammalian

subjects that exhibit ataxia and not present in a second population of subjects that do not exhibit ataxia.

7. The method of Claim 1 wherein the protein kinase C gamma gene is at least 90% identical to the nucleic acid sequence set forth in SEQ ID NO: 3.

8. The method of Claim 1 wherein the protein kinase C gamma gene is at least 95% identical to the nucleic acid sequence set forth in SEQ ID NO:3.

9. An isolated nucleic acid molecule encoding a protein kinase C gamma protein comprising a mutation selected from the group consisting of R41P, H101Y, S119P, Q127R, G128D, S361G and R597S.

10. An isolated nucleic acid molecule of Claim 9 which encodes the mutation R41P.

11. An isolated nucleic acid molecule of Claim 9 which encodes the mutation H101Y.

12. An isolated nucleic acid molecule of Claim 9 which encodes the mutation S119P.

13. An isolated nucleic acid molecule of Claim 9 which encodes the mutation Q127R.

14. An isolated nucleic acid molecule of Claim 9which encodes the mutation G128D.

15. An isolated nucleic acid molecule of Claim 9 which encodes the mutation S361G.

16. An isolated nucleic acid molecule of Claim 9 which encodes the mutation R597S.

17. A method of screening a mammalian subject to determine if said subject has a genetic predisposition to develop an ataxic neurological disease, or is suffering from an ataxic neurological disease, said method comprising analyzing the nucleic acid

sequence of a protein kinase C gamma gene in a mammalian subject to determine whether an identified genetic mutation that is associated with an ataxic neurological disease is present in the nucleic acid sequence, wherein the presence of an identified genetic mutation in the protein kinase C gamma gene that is associated with an ataxic neurological disease indicates that the mammalian subject has a genetic predisposition to develop an ataxic neurological disease or is suffering from an ataxic neurological disease.

18. The method of Claim 17 further comprising determining whether the mammalian subject is exhibiting ataxia.

19. The method of Claim 17 wherein said nucleic acid sequence is analyzed by a method selected from the group consisting of direct sequencing, sequencing PCR-amplified DNA, DNA hybridization, and restriction fragment length polymorphism.

20. The method of Claim 17 wherein said identified genetic mutation that is associated with ataxic neurological disease resides in exon 4 of the protein kinase C gamma gene.

21. The method of Claim 17 wherein said identified mutation is a missense mutation.

22. The method of Claim 17 wherein said identified mutation consists of an alteration in the protein kinase C gamma gene in the codon encoding an amino acid residue selected from the group consisting of amino acid residues 41, 101, 119, 127, 128, 361, and 597.

23. The method of Claim 22 wherein the alteration at protein position 41 is R41P.

24. The method of Claim 22 wherein the alteration at protein position 101 is H101Y.

25. The method of Claim 22 wherein the alteration at protein position 119 is S119P.

26. The method of Claim 22 wherein the alteration at protein position 127 is Q127R.

27. The method of Claim 22 wherein the alteration at protein position 128 is G128D.

28. The method of Claim 22 wherein the alteration at protein position 361 is S361G.

29. The method of Claim 22 wherein the alteration at protein position 597 is R597S.

30. A kit for determining susceptibility or presence of ataxic neurological disease in a mammalian subject based on the detection of a mutation in a protein kinase C gamma gene, said kit comprising (i) one or more nucleic acid primer molecules for amplification of a portion of a protein kinase C gamma gene and (ii) written indicia indicating a correlation between the presence of said mutation and risk of ataxic neurological disease.

31. The kit of Claim 30 further comprising means for determining whether a mutation associated with ataxic neurological disease is present.

32. The kit of Claim 30 further comprising nucleic acid primer molecules for sequencing across an amplified portion of a protein kinase C gamma gene.

33. The kit of Claim 30 further comprising control DNA.

34. The kit of Claim 30 wherein said mutation consists of an alteration in the nucleic acid sequence of protein kinase C gamma gene that encodes an amino acid residue selected from the group consisting of amino acid residues 41, 101, 119, 127, 128, 361, and 597.

35. The kit of Claim 30 wherein said mutation encodes R41P and wherein said primers comprise SEQ ID NO:4, SEQ ID NO:7 and SEQ ID NO:5.

36. The kit of Claim 30 wherein said mutation encodes H101Y and wherein said primers comprise SEQ ID NO:10, SEQ ID NO:11 and SEQ ID NO:13.

37. The kit of Claim 30 wherein said mutation encodes S119P and wherein said primers comprise SEQ ID NO:10, SEQ ID NO:11 and SEQ ID NO:13.

38. The kit of Claim 30 wherein said mutation encodes Q127R and wherein said primers comprise SEQ ID NO:10, SEQ ID NO:11 and SEQ ID NO:13.

39. The kit of Claim 30 wherein said mutation encodes G128D and wherein said primers comprise SEQ ID NO:10, SEQ ID NO:11 and SEQ ID NO:13.

40. The kit of Claim 30 wherein said mutation encodes S361G and wherein said primers comprise SEQ ID NO:20, SEQ ID NO: 21 and SEQ ID NO:23.

41. The kit of Claim 30 wherein said mutation encodes R597S and wherein said primers comprise SEQ ID NO: 32, SEQ ID NO:33 and SEQ ID NO:35.

42. The kit of Claim 30 wherein each primer molecule is identical to at least 10 contiguous nucleotides occuring in the sequence of the protein kinase C gamma gene disclosed in SEQ ID NO:3, or the complement thereof.